

**CRF Errors Corrected by the STIC Systems Branch**

09/05/01 PE # 6

Serial Number: 09/903,377

CRF Processing Date: 2/6/2002  
 Edited by: Am  
 Verified by: Am (STIC staff)

**ENTERED**

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

**\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

3/1/97

#6



OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/903,377

DATE: 02/06/2002  
TIME: 08:10:32

Input Set : N:\jumbos\903377.txt  
Output Set: N:\CRF3\02062002\I903377.raw

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4 <110> APPLICANT: Allen, Keith D.
6 <120> TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHEMOKINE
7   RECEPTOR 9A GENE DISRUPTIONS
10 <130> FILE REFERENCE: R-365
12 <140> CURRENT APPLICATION NUMBER: US 09/903,377
13 <141> CURRENT FILING DATE: 2001-07-10
15 <150> PRIOR APPLICATION NUMBER: US 60/217,255
16 <151> PRIOR FILING DATE: 2000-07-10
18 <150> PRIOR APPLICATION NUMBER: US 60/221,483
19 <151> PRIOR FILING DATE: 2000-07-27
21 <150> PRIOR APPLICATION NUMBER: US 60/262,113
22 <151> PRIOR FILING DATE: 2001-01-16
24 <160> NUMBER OF SEQ ID NOS: 4
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 2577
30 <212> TYPE: DNA
31 <213> ORGANISM: Artificial Sequence
33 <220> FEATURE:
34 <223> OTHER INFORMATION: Targeting vector
36 <400> SEQUENCE: 1
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38 gctgatgact atggctctga atccacatct tccatggaag actacgttaa cttcaacttc 120
39 actgacttct actgtgagaa aaacaatgtc aggcagtttg cgagccattt cctccacccc 180
40 ttgtactggc tctgtttcat cgtgggtgcc ttgggcaaca gtcttgttat ccttgcttac 240
41 tggtagtgca caagagtga gaccatgacc gacatgttcc ttttgaattt ggcaattgct 300
42 gacctcctct ttcttgtcac tcttcccttc tgggccattg ctgctgctga ccagtggagg 360
43 ttccagacct tcatgtgcaa ggtggtcaac agcatgtaca agatgaactt ctacagctgt 420
44 gtgttgctga tcatgtgcat cagcgtggac aggtacattg ccattgcccc ggccatgaga 480
45 gcacatactt ggaggagaaa aaggcttttg tacagcaaaa tggtttgctt taccatctgg 540
46 gtattggcag ctgctctctg catcccagaa atcttataca gccaaatcaa ggaggaaatcc 600
47 ggcattgcta tctgcaccat ggtttaccct agcgtatgaga gcaccaaact gaagtcagct 660
48 gtcttgaccc tgaaggtcat tctggggttc ttccttccct tctgtgtcat ggcttgctgc 720
49 tataccatca tcattcacac cctgatacaa gccaaagaat cttccaagca caaagcccta 780
50 aaagtgacca tcaactgtct gaccgtcttt gtcttgtctc agtttcccta caactgcatt 840
51 ttgttggtgc agaccattga cgcctatgcc atgttcatct ccaactgtgc cgtttccacc 900
52 aacattgaca tctgcttcca ggtcacccag accatgcctt tcttccacag ttgcctgaac 960
53 cctgtttctt atgtttttgt gggtagagaga ttccgcggg atctcgtgaa aacctgaag 1020
54 aacttgggtt gcatcagcca gggccagtgg gtttcattta caaggagaga ggaagcttg 1080
55 aagctgtcgt ctatgttgct ggagacaacc tcaggagcac tctccctctg aggggtcttc 1140
56 tctgaggtgc atggttcttt tggaagaaat gagaaataca tgaaacagtt tccccactga 1200
57 tgggaccaga gagagtgaag gagaaaagaa aactcagaaa gggatgaatc tgaactatat 1260
58 gattacttgt agtcagaatt tgccaaagca aatatttcaa aatcaactga ctagtgcagg 1320

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59 aggctgttga ttggtcttgg actgtgatgc ccgcaattct caaaggagga ctaaggaccg 1380
60 gcaactgtgga gcaccctggc ttgtccactc gccggagcat caatgccgct gcctctggag 1440
61 gagcccttgg attttctoca tgcactgtga acttctgtgg cttcagttct catgctgcct 1500
62 ctcccaaaag gggacacaga agcactggct gctgctacag accgcaaaag cagaaagttt 1560
63 cgtgaaaatg tccatctttg ggaaattttc taccctgctc ttgagcctga taacccatgc 1620
64 caggctcttat agattcctga tctagaacct ttccaggcaa tctcagacct aatttccttc 1680
65 tgttctcctt gttctgttct gggccagtga aggtccttgt tctgattttg aaacgatctg 1740
66 caggctcttgc cagtgaaccc ctggacaact gaccacaccc acaaggcatc caaagtctgt 1800
67 tggcttccaa tccatttctg tgtcctgctg gaggttttaa cctagacaag gattccgctt 1860
68 attccttggt atggtgacag tgtctctcca tggcctgagc agggagatta taacagctgg 1920
69 gttcgacagg gccagccttg gccctgttgt aggcctgttc tgttgagtg gacttgcttt 1980
70 gggtccaccg tctgtctgct ccctagaaaa tgggctggtt cttttggccc tcttctttct 2040
71 gaggcccaact ttattctgag gaatacagtg agcagatatg ggcagcagcc aggtagggca 2100
72 aaggggtgaa gcgcaggcct tgcctggaag ctatttactt ccatgcttct ccttttctta 2160
73 ctctatagtg gcaacatttt aaaagctttt aacttagaga ttaggctgaa aaaaataagt 2220
74 aatggaattc acctttgcat cttttgtgtc tttcttatca tgatttgga aaatgcatca 2280
75 cctttgaaaa tatttcacat attggaaaag tgctttttaa tgtgtatatg aagcattaat 2340
76 tacttgtcac tttctttacc ctgtctcaat attttaagt tgtgcaatta aagatcaaat 2400
77 agatacatta agagtgtgaa ggctggctctg aaggtagtga gctatctcaa tcggattgtt 2460
78 cacactcagt tacagattga actccttgtt ctacttcctt gcttctctct actgcaattg 2520
79 actagtcttt aaaaaaaagt gtgaagagta agcaataggg ataaggaaat aagatct 2577

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81 &lt;210&gt; SEQ ID NO: 2

82 &lt;211&gt; LENGTH: 357

83 &lt;212&gt; TYPE: PRT

84 &lt;213&gt; ORGANISM: Artificial Sequence

86 &lt;220&gt; FEATURE:

87 &lt;223&gt; OTHER INFORMATION: Targeting vector

89 &lt;400&gt; SEQUENCE: 2

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91 1 5 10 15
92 Val Asn Phe Asn Phe Thr Asp Phe Tyr Cys Glu Lys Asn Asn Val Arg
93 20 25 30
94 Gln Phe Ala Ser His Phe Leu Pro Leu Tyr Trp Leu Val Phe Ile
95 35 40 45
96 Val Gly Ala Leu Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys
97 50 55 60
98 Thr Arg Val Lys Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile
99 65 70 75 80
100 Ala Asp Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala
101 85 90 95
102 Ala Asp Gln Trp Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser
103 100 105 110
104 Met Tyr Lys Met Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile
105 115 120 125
106 Ser Val Asp Arg Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr
107 130 135 140
108 Trp Arg Glu Lys Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile
109 145 150 155 160
110 Trp Val Leu Ala Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln

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111                               165                               170                               175
112 Ile Lys Glu Glu Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser
113                               180                               185                               190
114 Asp Glu Ser Thr Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile
115                               195                               200                               205
116 Leu Gly Phe Phe Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile
117                               210                               215                               220
118 Ile Ile His Thr Leu Ile Gln Ala Lys Lys Ser Ser Lys His Lys Ala
119 225                               230                               235                               240
120 Leu Lys Val Thr Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe
121                               245                               250                               255
122 Pro Tyr Asn Cys Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met
123                               260                               265                               270
124 Phe Ile Ser Asn Cys Ala Val Ser Thr Asn Ile Asp Ile Cys Phe Gln
125                               275                               280                               285
126 Val Thr Gln Thr Ile Ala Phe Phe His Ser Cys Leu Asn Pro Val Leu
127                               290                               295                               300
128 Tyr Val Phe Val Gly Glu Arg Phe Arg Arg Asp Leu Val Lys Thr Leu
129 305                               310                               315                               320
130 Lys Asn Leu Gly Cys Ile Ser Gln Ala Gln Trp Val Ser Phe Thr Arg
131                               325                               330                               335
132 Arg Glu Gly Ser Leu Lys Leu Ser Ser Met Leu Leu Glu Thr Thr Ser
133                               340                               345                               350
134 Gly Ala Leu Ser Leu
135                               355
138 <210> SEQ ID NO: 3
139 <211> LENGTH: 200
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Targeting vector
146 <400> SEQUENCE: 3
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148 tccacagatg actacatgaa ttggaatttc agtagcttct tctgtaagaa aaataatgtc 120
149 aggcagtttg caagccattt tctcccacct ctgtactggc ttgtgttcat tgtgggcacc 180
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152 <210> SEQ ID NO: 4
153 <211> LENGTH: 200
154 <212> TYPE: DNA
155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: Targeting vector
160 <400> SEQUENCE: 4
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162 acattgccat tgtacaggcc atgaaggctc aggtctggag gcagaaaagg ccgctataca 120
163 gcaagatggc ctgcattacc atctgggtga tggcagctgt gctctgcacc ccagaaatcc 180
164 tgtacagtca agtcagtggg                               200

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VERIFICATION SUMMARY

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